



## SEQUENCE LISTING

<110> Eck, Jorgen  
Schmidt, Arno  
Zinke, Holger

<120> Recombinant Fusion Proteins Based on  
Ribosome-Inactivating Proteins of the mistletoe Viscum  
album

<130> 09282-5

<140> 09/347,064

<141> 1999-07-02

<150> PCT/EP98/00009

<151> 1998-01-02

<150> EP 97 10 0012.0

<151> 1997-01-02

<160> 38

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

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ctcttgctgc agtctacgat ccccgctctcc gatgcgcaaa gatttgcttt ggtggagctc 180  
accaaccagg ggggagactc gatcacggcc gccatcgacg ttaccaatct gtacgtcgtg 240  
gcttaccaag caggcgacca atcctacttt ttgcgcgacg caccacgcgg cgcggaaacg 300  
catctcttca ccggcaccac ccgatactct ctccattca acggaagcta cctgatctg 360  
gagcgatacg ccggacatag ggaccagatc cctctcggtg tagaccaact cattcaatcc 420  
gtcacggcgc ttcgttttcc gggcggcagc acgcgtaccc aagctcgttc gattttaatc 480  
ctcattcaga tgatctccga ggccgccaga ttcaatccca tcttatggag ggctcgccaa 540  
tacattaaca gtggggcgctc atttctgccg gacgtgtaca tgctggagct ggagacgagt 600  
tggggccaac aatccacgca agtccagcat tcaaccgatg gcgtttttaa taaccaatt 660  
cggttggcta taccctccgg taacttcgtg acgttgacca atgttcgcga cgtgatcgcc 720  
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<210> 2

<211> 252

<212> PRT

<213> Viscum album

<400> 2

Met Tyr Glu Arg Ile Arg Leu Arg Val Thr His Gln Thr Thr Gly Glu  
1 5 10 15

Glu Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly  
20 25 30

Ser Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val  
35 40 45

Ser Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly  
 50 55 60  
 Asp Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala  
 65 70 75 80  
 Tyr Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly  
 85 90 95  
 Ala Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe  
 100 105 110  
 Asn Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln  
 115 120 125  
 Ile Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg  
 130 135 140  
 Phe Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu  
 145 150 155 160  
 Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg  
 165 170 175  
 Ala Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr  
 180 185 190  
 Met Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln  
 195 200 205  
 His Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro  
 210 215 220  
 Pro Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser  
 225 230 235 240  
 Leu Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro  
 245 250

<210> 3  
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 <213> Viscum album

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 aggcctgtga tagccgatga tgttacatgt agtgcttcgg aacctacggt gcggattgtg 60  
 ggtcgaaatg gcatgtgcgt ggacgtccga gatgacgatt tccgcgatgg aaatcagata 120  
 cagttgtggc cctccaagtc caacaatgat ccgaatcagt tgtggacgat caaaagggat 180  
 ggaaccattc gatccaatgg cagctgcttg accacgtatg gctatactgc tggcgtctat 240  
 gtgatgatct tcgactgtaa tactgctgtg cgggaggcca ctctttggca gatatggggc 300  
 aatggggacca tcatcaatcc aagatccaat ctggtttttg cagcatcatc tggaatcaaa 360  
 ggcactacgc ttacgggtgca aacactggat tacacgtttg gacagggtcg gcttgccggt 420  
 aatgataccg cccacgcga ggtgaccata tatgggttca gggacctttg catggaatca 480  
 aatggaggga gtgtgtgggt ggagacgtgc gtgagtagcc aaaagaacca aagatgggct 540  
 ttgtacgggg atggttctat acgccccaaa caaaaccaag accaatgcct cacctgtggg 600  
 agagactccg tttcaacagt aatcaatata gttagctgca gcgctggatc gtctgggcag 660  
 cgatgggtgt ttaccaatga aggggccatt ttgaatttaa agaattgggt ggccatggat 720  
 gtggcgcaag caaatccaaa gctccgccga ataatcatct atcctgccac agggaaacca 780

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828

<210> 4

<211> 267

<212> PRT

<213> Viscum album

<400> 4

Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly  
1 5 10 15

Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Asp Phe Arg Asp Gly  
20 25 30

Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln  
35 40 45

Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys  
50 55 60

Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp  
65 70 75 80

Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn  
85 90 95

Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser  
100 105 110

Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu  
115 120 125

Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr  
130 135 140

Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val  
145 150 155 160

Trp Val Glu Thr Cys Val Ser Ser Gln Lys Asn Gln Arg Trp Ala Leu  
165 170 175

Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu  
180 185 190

Thr Cys Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys  
195 200 205

Ser Ala Gly Ser Ser Gly Gln Arg Trp Val Phe Thr Asn Glu Gly Ala  
210 215 220

Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala Asn  
225 230 235 240

Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro Asn  
245 250 255

Gln Met Trp Leu Pro Val Pro Gly Gly Tyr His  
260 265

<210> 5  
 <211> 72  
 <212> DNA  
 <213> Viscum album

<400> 5  
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 gatgttacat gt 72

<210> 6  
 <211> 17  
 <212> PRT  
 <213> Viscum album

<400> 6  
 Ser Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile  
 1 5 10 15  
 Ala

<210> 7  
 <211> 756  
 <212> DNA  
 <213> Viscum album

9  
 <400> 7  
 tacgaacgta tccgtctgcg tgttacccac cagaccaccg gtgaagaata tttccgggttc 60  
 atcacgcttc tccgagatta tgtctcaagc ggaagctttt ccaatgagat accactcttg 120  
 cgtcagtcta cgatccccgt ctccgatgcy caaagatttg tcttgggtgga gctcaccac 180  
 cagggggggag actcgatcac ggccgccatc gacgttacca atctgtacgt cgtgggttac 240  
 caagcaggcg accaatccta ctttttgcyg gacgcaccac gcggcgcgga aacgcatttc 300  
 ttcaccggca ccacccgatc ctctctccca ttcaacggaa gctaccctga tctggagcga 360  
 tacgccggac atagggacca gatccctctc ggtatagacc aactcattca atccgtcacg 420  
 gcgcttcggt ttcggggcgg cagcacgcgt acccaagctc gttcgatttt aatcctcatt 480  
 cagatgatct ccgaggccgc cagattcaat cccatcttat ggagggctcg ccaatacatt 540  
 aacagtgggg cgtcatttct gccagacgtg tacatgctgg agctggagac gagttggggc 600  
 caacaatcca cgcaagtcca gcattcaacc gatggcggtt ttaataaccc aattcggttg 660  
 gctatacccc ccggttaact cgtgacgttg accaatgttc gcgacgtgat cgccagcttg 720  
 gcgatcatgt tgtttgtatg cggagagcgg ccatct 756

<210> 8  
 <211> 252  
 <212> PRT  
 <213> Viscum album

<400> 8  
 Tyr Glu Arg Ile Arg Leu Arg Val Thr His Gln Thr Thr Gly Glu Glu  
 1 5 10 15  
 Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly Ser  
 20 25 30  
 Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser  
 35 40 45  
 Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly Asp  
 50 55 60

Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala Tyr  
 65 70 75 80  
 Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly Ala  
 85 90 95  
 Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn  
 100 105 110  
 Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile  
 115 120 125  
 Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe  
 130 135 140  
 Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile  
 145 150 155 160  
 Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala  
 165 170 175  
 Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met  
 180 185 190  
 Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln His  
 195 200 205  
 Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro  
 210 215 220  
 Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu  
 225 230 235 240  
 Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro Ser  
 245 250

<210> 9  
 <211> 789  
 <212> DNA  
 <213> Viscum album

<400> 9  
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 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc 180  
 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240  
 tgaataactg ctgtgcggga ggccactctt tggcagatat ggggcaatgg gaccatcatc 300  
 aatccaagat ccaatctggt tttggcagca tcactctggaa tcaaaggcac tacgcttacg 360  
 gtgcaaacac tggattacac gttgggacag ggctggcttg ccgtaatatg taccgcccc 420  
 cgcgaggtga ccatatatgg gttcaggac ctttgcattg aatcaaatgg agggagtgtg 480  
 tgggtggaga cgtgcgtgag tagccaaaag aaccaaagat gggctttgta cggggatggt 540  
 tctatacgcc ccaaacaaaa ccaagaccaa tgcctcacct gtgggagaga ctccgtttca 600  
 acagtaatca atatatgttag ctgcagcgct ggatcgctg ggcagcgatg ggtgtttacc 660  
 aatgaagggg ccattttgaa tttaaagaat gggttggcca tggatgtggc gcaagcaaat 720  
 ccaaagctcc gccgaataat catctatcct gccacaggaa aaccaaataa aatgtggctt 780  
 cccgtgccca 789

<210> 10

<211> 263  
 <212> PRT  
 <213> Viscum album

<400> 10

Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly  
 1 5 10 15

Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Asp Phe Arg Asp Gly  
 20 25 30

Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln  
 35 40 45

Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys  
 50 55 60

Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp  
 65 70 75 80

Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn  
 85 90 95

Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser  
 100 105 110

Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu  
 115 120 125

Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr  
 130 135 140

Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val  
 145 150 155 160

Trp Val Glu Thr Cys Val Ser Ser Gln Lys Asn Gln Arg Trp Ala Leu  
 165 170 175

Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu  
 180 185 190

Thr Cys Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys  
 195 200 205

Ser Ala Gly Ser Ser Gly Gln Arg Trp Val Phe Thr Asn Glu Gly Ala  
 210 215 220

Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala Asn  
 225 230 235 240

Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro Asn  
 245 250 255

Gln Met Trp Leu Pro Val Pro  
 260

<210> 11  
 <211> 48  
 <212> DNA

<213> Viscum album

<400> 11

tcctctgagg tgcgctattg gccgctggtc atacgaccgc tgatagcc

48

<210> 12

<211> 16

<212> PRT

<213> Viscum album

<400> 12

Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile Ala  
1 5 10 15

<210> 13

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic gene  
encoding amino acids 53-78 of human P2 protein

<400> 13

gtaccgggtg gcggtcgtag cgaatccacc ttcaaaaaca ccgaaatctc cttcaaactg 60  
ggtcaggaat tcgaagaaac caccgctgac aact 94

<210> 14

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino acids  
53-78 of human P2 protein

<400> 14

Arg Thr Glu Ser Thr Phe Lys Asn Thr Glu Ile Ser Phe Lys Leu Gly  
1 5 10 15

Gln Glu Phe Glu Glu Thr Thr Ala Asp Asn  
20 25

<210> 15

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 20:  
Synthetic linker cassette for providing modularity  
at the 3' end of rMLB delta 1alpha 1beta

<400> 15

caccggtaaa ccgaaccaga tgtggctgcc ggtaccgtag taacgctcct cgtcgaccta 60  
gtaaggatcc ctcga 75

<210> 16  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 20: amino  
 acid sequence encoded by portion of SEQ ID NO: 15

<400> 16  
 Thr Gly Lys Pro Asn Gln Met Trp Leu Pro Val Pro  
           1                  5                  10

<210> 17  
 <211> 82  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 21:  
 Synthetic linker cassette for providing modularity  
 at the 3'end of rMLB Delta 1alpha 1beta 2gamma  
 with affinity module ("His-Tag").

g  
 <400> 17  
 ccggtaaacc gaaccagatg tggctgccgg taccgggtgg tggatatcat caccaccatc 60  
 accactagta actcctcgga tc 82

<210> 18  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Amino acid  
 sequence encoded by a portion of SEQ ID NO: 17

<400> 18  
 Gly Lys Pro Asn Gln Met Trp Leu Pro Val Pro Gly Gly Gly Tyr His  
           1                  5                  10                  15

His His His His His  
                   20

<210> 19  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Codon exchange  
 rMLB D23A

<400> 19  
 catgtgcgtg gccgtccgag atgacg 26



<210> 20  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 22:  
 Mutagenic oligonucleotides for inactivating  
 carbohydrate binding sites in rMLB. - 1alpha2  
 (W38A). -

<400> 20  
 cagatacagt tggcgccctc caagtcc

27

<210> 21  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 22:  
 Mutagenic oligonucleotides for inactivating  
 carbohydrate binding sites in rMLB. - 1beta (Y68S,  
 Y70S, Y75S, F79S). -

9  
 <400> 21  
 gctgcttgac cacgtctggc tctactgctg gcgtctctgt gatgatctcc gactgtaata 60  
 c 61

<210> 22  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 22:  
 Mutagenic oligonucleotides for inactivating  
 carbohydrate binding sites in rMLB. - 1beta1  
 (D235A). -

<400> 22  
 ggggttgcca tggctgtggc gcaagc

26

<210> 23  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 22  
 Mutagenic oligonucleotides for inactivating  
 carbohydrate binding sites in rMLB. - 2gamma2  
 (Y249A). -

<400> 23

cgaataatca tcgctcctgc cacagg

26

<210> 24

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 22:  
Mutagenic oligonucleotides for inactivating  
carbohydrate binding sites in rMLB. - pT7 EcoRV to  
SspI. -

<400> 24

cttccttttt caatattatt gaagcattta tcagg

35

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 22:  
Mutagenic oligonucleotides for inactivating  
carbohydrate binding sites in rMLB. - pT7 SspI to  
EcoRV. -

<400> 25

cttccttttt cgatatcatt gaagcattta tcagg

35

<210> 26

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 23:  
Mutagenic oligonucleotides for constructing  
modular ITF gene cassettes. - pT7 Delta NdeI to  
StuI. -

<400> 26

ctttaagaag gagatataca ggcctacgag aggctaagac

40

<210> 27

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 23:  
Mutagenic oligonucleotides for constructing  
modular ITF gene cassettes. - rMLB silent NheI. -

<400> 27

gttacctgca gtgctagcga acctacggtg cgg

33

<210> 28  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 23:  
 Mutagenic oligonucleotides for constructing  
 modular ITF gene cassettes. - rMLA Delta AgeI. -

<400> 28  
 cccaccagac caccggcgaa gaatatttcc gg 32

<210> 29  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 23:  
 Mutagenic oligonucleotides for constructing  
 modular ITF gene cassettes.

<400> 29  
 gtttgtatgc ggagagcgtc cctcgagctc tgaggtgcgc 40

9  
 <210> 30  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Fig. 23:  
 Mutagenic oligonucleotides for constructing  
 modular ITF gene cassettes. - rMLB Delta EcoNI to  
 AgeI. -

<400> 30  
 ccgaataatc atcgctccgg ccaccggtaa accaaatcaa atg 43

<210> 31  
 <211> 11  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Flanking region  
 of the ProML gene cassette in expression vector  
 pT7ProML

<400> 31  
 tacatatgta c 11

<210> 32

<211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Flanking region  
 of the ProML gene cassette in expression vector  
 pT7ProML

<400> 32  
 ccatgataag gatcctctag 20

<210> 33  
 <211> 9  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Flanking region  
 of the IML gene cassette in expression vector  
 PIML-02-P

<400> 33  
 caggcctac 9

9  
 <210> 34  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Flanking region  
 of the IML gene cassette in expression vector  
 PIML-02-P

<400> 34  
 cactagtaac tcctcggatc ctctagagtc gacc 34

<210> 35  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Modulator  
 module peptide

<400> 35  
 Lys Asp Glu Leu  
 1

<210> 36  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Modulator  
module peptide

<400> 36

His Asp Glu Leu

1

<210> 37

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Portion of the  
ML propeptide

<400> 37

Ser Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile  
1 5 10 15

Ala

<210> 38

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:A degradation  
product of myelin basic protein.

<400> 38

Val His Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro  
1 5 10